

Allele Frequency Activity

Introduction

Lactase persistence is the genetic ability to keep producing the lactase enzyme as an adult, allowing for the lifelong digestion of lactose in milk. Most mammals lose this ability after weaning, which leads to lactose intolerance. However, mutations have occurred within the lactase gene over the last 10,000 years that have maintained the expression of this protein within humans. Lactase persistence is more common in European populations with higher levels of domesticated cows (where milk is available).

Aim

To determine the relationship between the frequency of lactase persistence and European settlement

Hypothesis

Using the theory of natural selection, explain why lactase persistence is more common in Europeans

Materials

- Interactive world map of lactase persistence: <https://coblabugr.shinyapps.io/lactasepersistence/>

Method

1. Access the interactive world map of lactase persistence and select 'phenotype frequencies'
2. For each selected region, select the clusters identified below and record the phenotype frequency

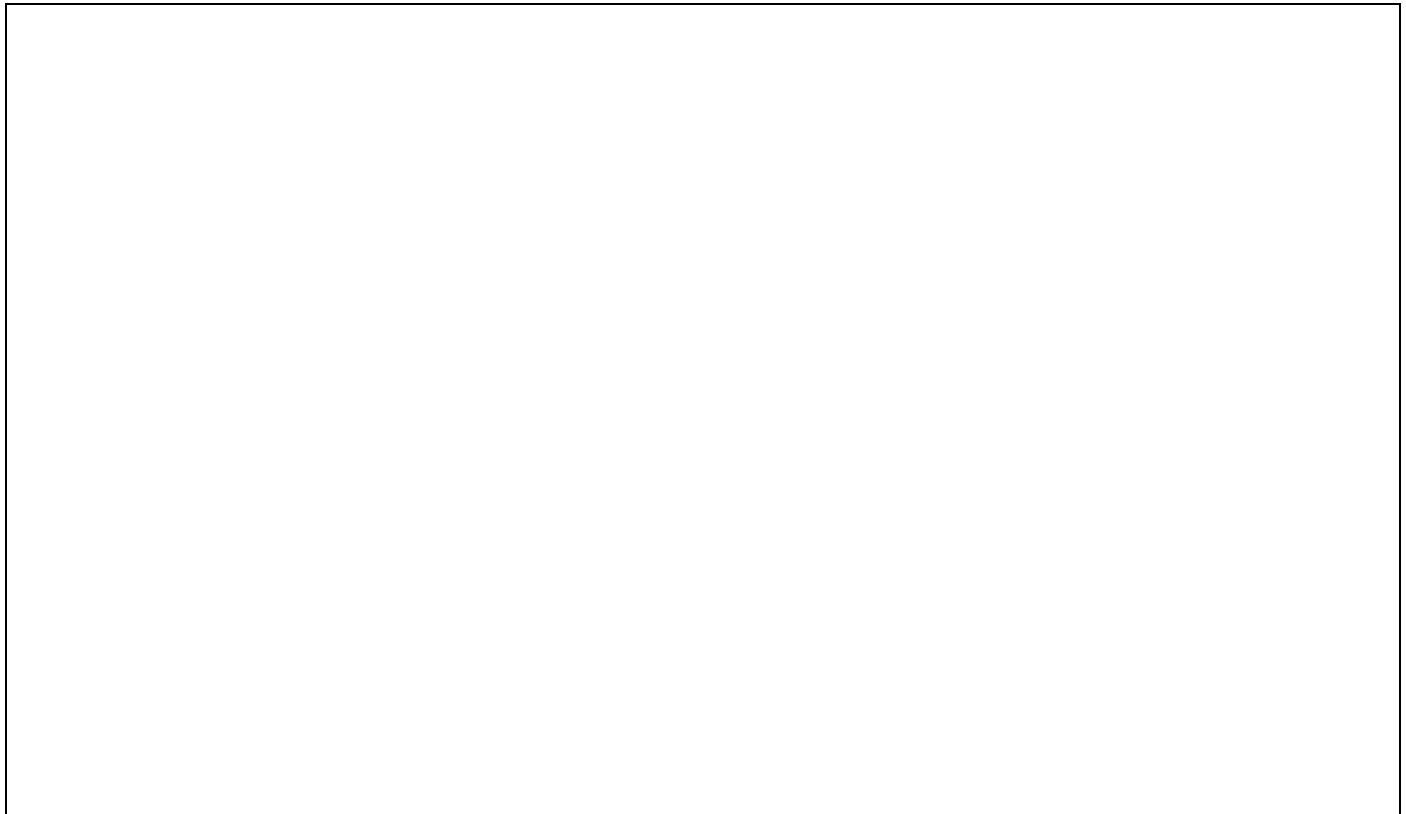
| Region | <i>Europe</i> | <i>America</i> | <i>Africa</i> | <i>Asia</i> |
|-----------|--|--|--|--|
| Expansion | Norman Conquest | Age of Discovery | New Imperialism | Decolonisation Era |
| Time | 1066 | 1492 | 1885 | 1945 |
| Clusters | United Kingdom Norway Germany France Spain | United States Canada Mexico Brazil Uruguay | South Africa Nigeria Somalia Kenya Algeria | China Japan Thailand Mongolia Malaysia |

Results – Raw Data

| | Europe | America | Africa | Asia |
|-------------------------------|--------|---------|--------|------|
| Phenotype Frequencies (Ratio) | | | | |
| | | | | |
| | | | | |
| | | | | |
| | | | | |
| Mean | | | | |

Results – Processed Data

1. Chart the data points on a scattergram (Time of Expansion vs Mean Phenotype Frequency)



2. Use Excel to calculate a correlation coefficient for this data



Discussion

1. Describe the trend between frequency of lactase persistence and widespread European migration

2. Suggest reasons for the variations seen between the different clusters within each region

3. What additional data could be used to improve the validity of your experimental findings

4. Distinguish between phenotype frequency and allele frequency